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Big Data Pipeline Unit

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NORTH DAKOTA STATE UNIVERSITY

# BIG DATA PIPELINE

*Automation, data management, analytics*





**40 Million acres**

**Avg farm size ~ 1,500 acres**

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# 42 Commodities



**Generates \$7.6 billion in  
cash receipts annual**

# NDSU Presenters



## **DIDIER MURILLO FLOREZ**

Research Statistician  
Developer

Didier is a Mathematician and Statistician leading the development of statistical applications and algorithms that simplify end-user workflows at the ND AES Big Data Pipeline Unit. He is the main developer of FieldHub.



## **MATTHEW SEEFELDT**

Software Development &  
Media Content Creator

Matthew is a Mathematician creating R-Shiny applications for our team. Additionally he develops multi-media projects for teaching tools for all our audiences. Main contributions made to FieldHub and Athena.



## **ANA MARIA HEILMAN**

Senior Big Data Pipeline  
Manager

Ana is leading a growing team of data scientist, software developers, statisticians/mathematicians and bioinformaticist that support the ND Agricultural Experiment Station.

# Main Contributors



## **RICHARD HORSLEY**

Barley Breeder & Head  
Department of Plant Sciences

Richard is a plant breeder with more than 40+ years of experience in plant breeding, experimental design, analysis of data, and academic administration. He is one of the minds behind the tools and technologies we develop in our team.



## **JOHAN APARICIO**

Research Associate  
Statistician, CIAT

Johan is a Statistician leading the development of statistical applications and tools used by different research units at the International Center for Tropical Agriculture (CIAT). He is the main developer of Mr.Bean

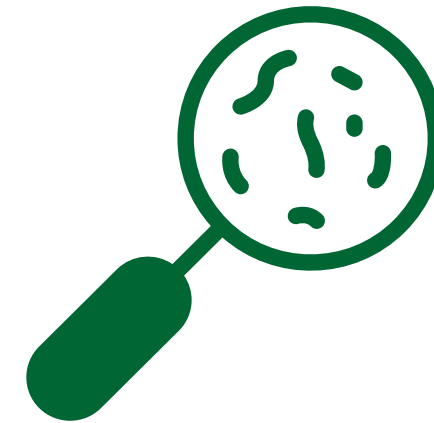
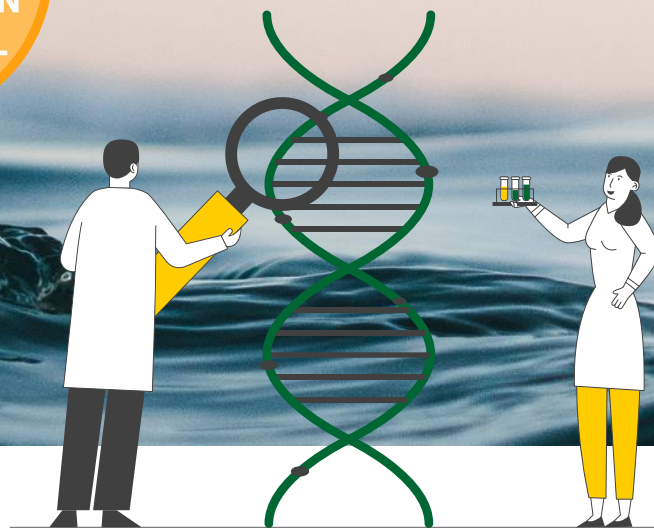
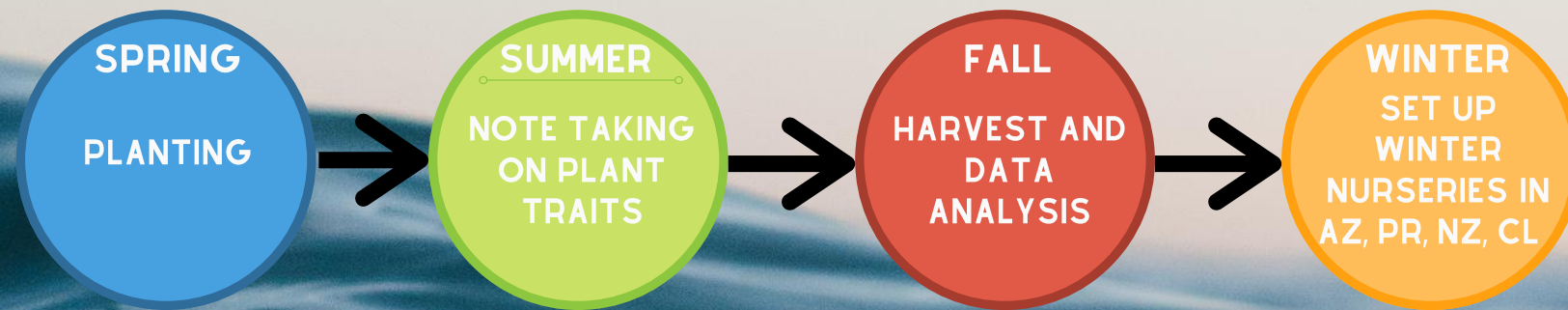


## **SALVADOR GEZAN**


Statistical Genetics  
Consultant, VSNi

Salvador is a Quantitative Geneticist and Plant Breeder, who is an Affiliate Faculty for the Department of Plant Sciences at NDSU. He is a contributor to both FieldHub and Mr.Bean applications, and also provides guidance to our team in analytic related projects.

# Building Pipelines and Apps to Accelerate Discovery



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# Introduction to Design Of Experiments

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# **What is Experimental Error?**

**5-10 word definition...**

**“Differences in experimental units treated alike”**

**An appropriate field experimental design should help you to:**

**1- Minimize Exp. Error**

**2- Measure the existing Exp. error**

# How to set up correctly your experiment?

**1. Randomization**

**1. Replication**

**1. Blocking**

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Randomization is widely recognized as a basic principle of statistical experimentation

# Randomization



- Reduces the bias
- Allows statistical tests
- Improves the accuracy in results

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# Replication

Increase the **precision**

Reduces **uncertainty**

Separates **background noise**

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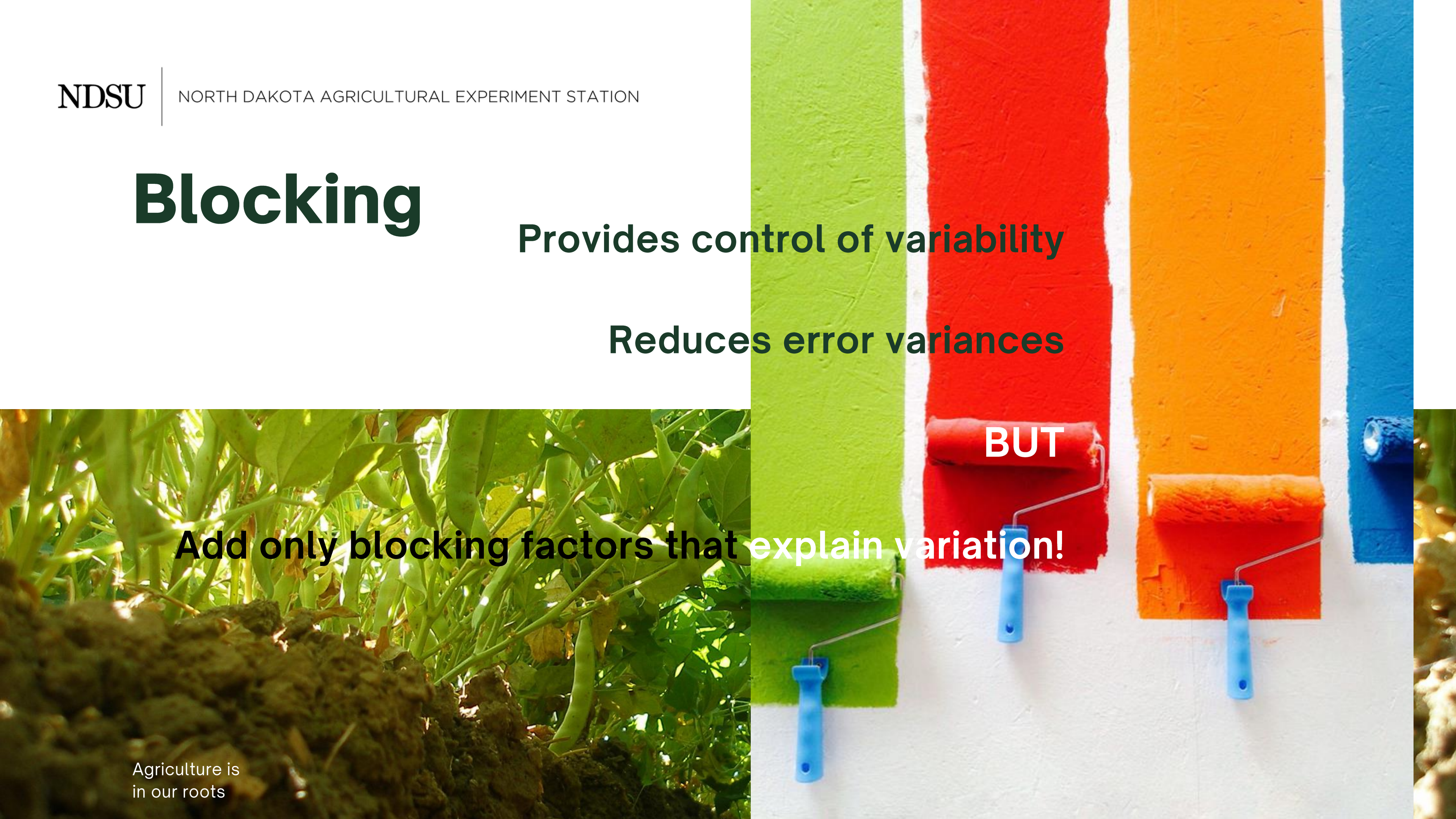
# Blocking

Provides control of variability

Reduces error variances

**BUT**

**Add only blocking factors that explain variation!**



# DOE in Agriculture and Plant Breeding

The origins of DOE comes from experiments in agriculture. There are a variety of applications in different areas such as soil science, weed science, plant breeding, and precision agriculture among many others.

- Discard/select new genotypes in plant breeding programs
- Compare fertilizer effects under different irrigations systems
- Evaluate plant response under heat stress
- Compare precision agriculture methods

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# Recap

01

Randomization

02

Replication

03

Blocking

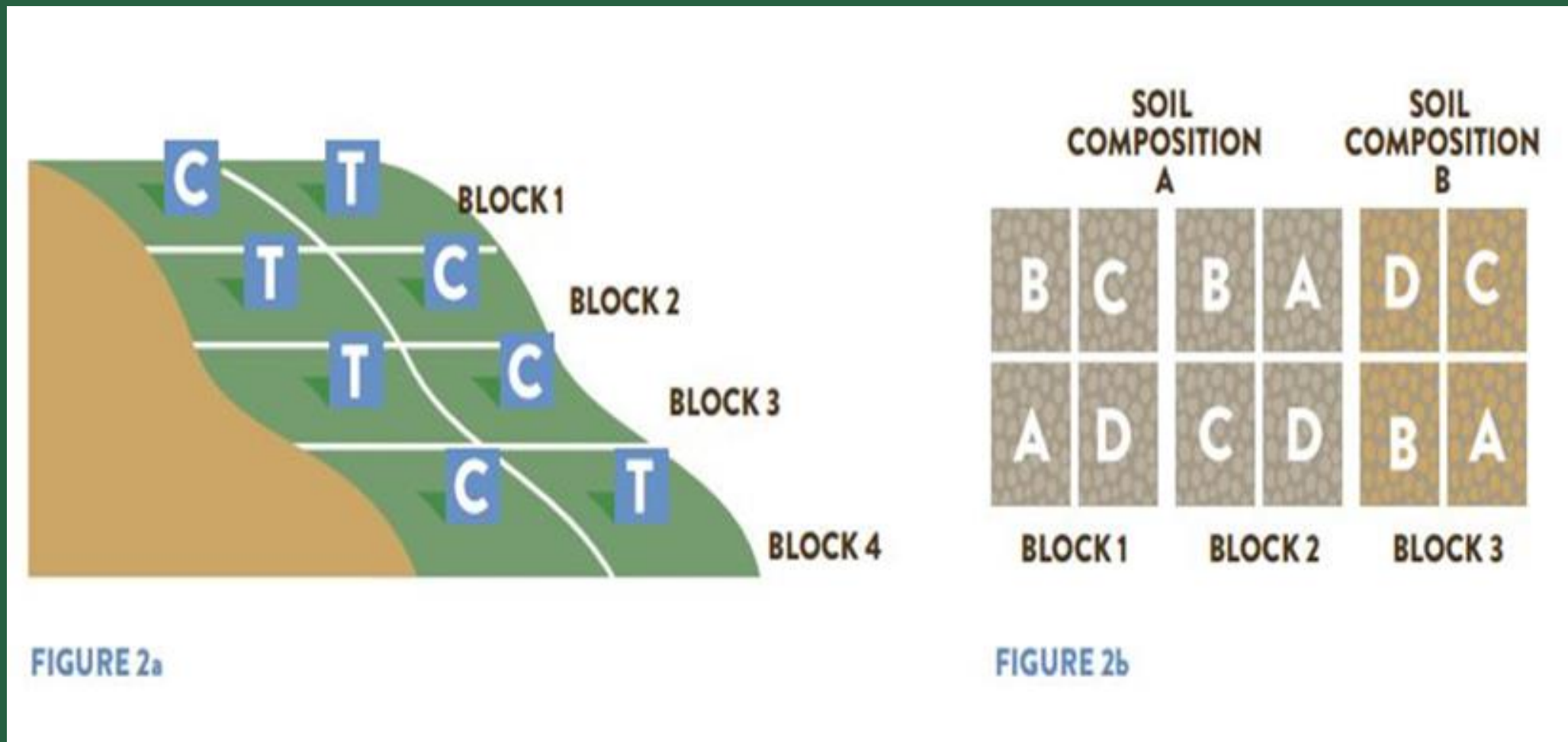


Figure from: <https://www.sare.org/wp-content/uploads/how-to-conduct-research-on-your-farm-or-ranch.pdf>

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Field Heterogeneity

# Spatial Correlation in field trials designs

- The experimental field is never completely homogeneous.
- Even before the plants are established in the field plots, there is some level of variability in soil properties.
- Experimental units that are closer together tend to be more similar than plots that are separated by greater distances.
- Row and column data are utilized to explain spatial variability in the field.



DOE

# Experimental Designs in Agriculture (especially Plant Breeding)

- Randomized Complete Block Design (RCBD)
- Augmented RCBD
- Alpha-Lattice Design
- Partially Replicated Designs (prep)
- Unreplicated designs



# Randomized Complete Block Design (RCBD)

- Each of the  $v$  treatments occurs once in every block (or replicate), and the number of units per block,  $k$ , is equal to the number of treatments ( $v=k$ ).
- Advantage: balanced dataset, i.e. all treatment comparison has the same precision.
- Consider a study where we want to design an experiment with  $v = 18$  treatments, where each will be replicated  $r = 3$  times.

Randomized Complete Block Design 9X6

T10	T13	T1	T5	T11	T4
T7	T15	T17	T14	T3	T2
T12	T6	T9	T8	T18	T16
T15	T18	T14	T17	T9	T5
T3	T4	T1	T16	T10	T2
T7	T11	T8	T13	T12	T6
T12	T6	T10	T9	T18	T14
T11	T15	T3	T16	T5	T8
T4	T7	T1	T2	T13	T17

ROWS

COLUMNS





# Alpha-Lattice Design

- When several treatments are evaluated, blocks can become quite large, and experimental units within the block are no longer homogeneous.
- Particularly recommended in cases where the number of treatments is large.
- Considering the example with 80 treatments, 3 reps and 5 units per incomplete block.

Alpha Lattice Design Field Layout 15X16

51	64	36	37	3	57	60	18	69	33	70	59	79	72	17	54
14	6	67	24	23	74	15	63	66	4	8	5	11	43	58	75
73	62	39	68	45	35	22	65	13	40	49	38	46	7	55	19
56	80	25	31	29	9	42	20	16	41	50	30	48	10	61	28
47	77	52	12	32	21	76	26	27	1	78	2	44	71	34	53
40	44	50	29	48	16	53	51	46	72	60	78	52	28	54	14
36	65	9	33	35	6	37	38	5	73	18	25	10	55	63	23
45	30	4	15	17	76	66	71	8	69	31	56	75	41	11	34
2	7	61	79	32	70	64	42	43	58	47	20	3	21	22	49
12	19	68	80	39	59	67	74	26	1	62	77	27	13	57	24
1	14	62	68	5	66	56	39	7	51	22	29	13	42	40	11
74	10	69	28	80	17	79	72	78	65	30	43	49	26	27	70
77	41	19	25	52	33	2	54	12	36	64	21	38	53	8	3
44	6	32	46	34	71	9	31	15	61	23	67	48	45	60	73
24	63	50	76	57	20	75	59	55	16	4	47	18	58	35	37

# Partially Replicated Design

Designs where:

- A portion of treatments are replicated two or three times.
- The rest of the plots are considered for unreplicated treatments.
- Consider an example with: 225 treatments, 75 treatments appear twice and the rest 150 appear just one time.

Partially Replicated Design 15 x 20

	34	155	77	178	196	150	12	20	69	37	99	58	108	162	87	1	179	52	19	60
	35	146	50	57	79	65	43	223	74	144	205	147	70	9	82	212	113	125	180	137
	27	192	177	182	52	132	211	10	117	163	111	204	207	44	51	4	53	121	184	25
	5	2	22	219	114	72	67	29	202	104	53	55	18	30	39	152	159	43	94	66
	116	68	14	122	49	42	169	133	4	218	160	23	64	96	6	24	120	86	18	61
	40	33	134	209	49	157	3	168	35	26	17	48	27	69	154	203	56	161	170	73
	167	143	130	11	13	45	30	36	7	181	74	63	2	38	61	67	54	57	55	142
	195	72	8	118	138	107	62	95	64	136	15	158	89	173	47	51	63	40	76	191
	145	19	39	13	80	176	101	25	44	221	32	153	199	59	213	110	46	131	28	7
	14	12	216	33	16	75	91	214	105	128	148	10	97	200	172	194	21	11	88	140
	127	165	198	32	164	62	6	124	103	21	50	78	93	225	31	83	175	210	45	66
	186	1	24	23	60	220	58	26	119	37	100	3	92	28	36	34	166	188	149	112
	84	48	90	208	115	20	217	70	201	9	71	102	22	197	193	38	174	135	141	189
	98	185	65	171	187	139	190	81	126	56	183	5	46	8	129	206	68	17	54	106
	31	224	42	73	59	85	109	29	71	41	75	222	15	215	16	156	123	41	47	151

# Unreplicated Designs With Checks

Designs where:

- A large number of entries are unreplicated together with a group (usually 3 or 4) of check genotypes that are replicated in order to capture and model potential field effects.
- They enable the evaluation of a large number of genotypes (entries) in those cases with limited quantities of seed.
- Several arrangements exist: random, diagonal, optimized

Un-replicated Diagonal Arrangement 16 x 20

247	2	167	229	76	79	22	46	205	2	206	31	230	16	176	62	126	3	278	152
149	270	253	181	2	130	7	114	244	173	17	81	2	137	106	49	277	84	127	273
191	128	15	261	164	156	103	1	5	141	190	63	284	240	269	1	174	25	160	222
162	215	1	28	235	27	40	9	165	255	4	138	45	148	35	276	219	111	3	119
64	256	30	281	26	3	267	24	10	258	187	82	60	4	68	109	32	90	239	50
4	204	87	271	144	225	196	241	1	36	245	142	192	33	131	43	2	20	200	89
42	100	237	1	212	280	139	199	231	182	73	4	184	168	56	178	155	117	124	2
195	77	234	66	198	57	3	107	242	260	248	185	217	145	3	18	147	12	140	61
179	4	169	58	54	83	194	65	14	1	37	272	47	150	268	251	122	1	158	283
104	80	101	249	4	102	41	59	44	186	38	39	3	105	125	226	75	197	69	108
218	211	29	74	282	34	171	1	202	115	151	8	193	243	210	2	159	264	180	236
129	153	3	110	95	203	170	161	67	85	3	11	92	177	189	172	232	88	1	98
209	123	86	224	52	4	201	275	99	157	94	55	254	2	207	19	53	6	257	143
4	48	112	96	259	279	113	21	4	252	223	71	274	146	175	116	2	216	51	78
233	166	188	2	134	227	135	263	133	120	136	3	228	250	154	132	70	221	118	3
266	93	163	121	91	213	4	72	13	214	265	208	23	220	1	246	262	238	97	183

Multomic analyses in plant breeding

# Designing & Analyzing Your Experiments Using FieldHub & Mr.Bean

Presented by Big  
Data Pipeline Team  
Didier Murillo Florez  
Matthew Seefeldt  
Johan Aparicio  
Ana Maria Heilman





Part 3:

# FieldHub

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Date:  
Sept 29, 2022



# What is FieldHub

- FieldHub is an R package/Shiny app that allows creating randomizations for a variety of experimental designs with applications in agriculture, plant breeding, forestry, animal, and biological sciences.
- The Big Data Pipeline Unit at NDSU is in charge of the development and maintenance of FieldHub. The app release was on May 2021 at CRAN. Recently, the team released a second version with new features.



# FieldHub

## Sources



GitHub: <https://github.com/DidierMurilloF/FieldHub>



CRAN: <https://cran.r-project.org/web/packages/FieldHub/index.html>



Web Page: <https://didiermurillof.github.io/FieldHub/>



JOSS Paper: <https://joss.theoj.org/papers/10.21105/joss.03122>



YouTube: <https://www.youtube.com/watch?v=Q9bftid0kPw&t=75s>



# Questions



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# Thank you

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